

**Amendments to the Sequence Listing:**

The attached sequence listing on sheets 1/13 – 13/13 is amended at heading line <110> to correctly identify the applicants. The sequences are not amended.

Attachment: Replacement sheets 1/13 to 13/13

## SEQUENCE LISTING

<110> Genesis Group Inc., Kenneth Kao, Catherine Popadiuk

<120> Pygopus in Diagnosis and Treatment of Cancer

<130> 50680-4

<150> US 60/463 309

<151> 2003-04-17

<150> US 60/496 012

<151> 2003-08-19

<160> 28

<170> PatentIn version 3.3

<210> 1

<211> 3190

<212> DNA

<213> homosapiens

<220>

<223> hPygo-2

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<221> CDS

<222> (173)..(1393)

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ccaagggcgc ctccatcccc cgccgctgcc gctaaccgg gtcccccact cc atg gcc	178
Met Ala	
1	
gcc tcg gcg ccc cca ccg gac aag ctg gag gga ggt ggc ggc ccc	226
Ala Ser Ala Pro Pro Pro Pro Asp Lys Leu Glu Gly Gly Gly Pro	
5 10 15	
gca ccg ccc cct gcg ccg ccc agc acc ggg agg aag cag ggc aag gcc	274
Ala Pro Pro Pro Ala Pro Pro Ser Thr Gly Arg Lys Gln Gly Lys Ala	
20 25 30	
ggt ctg caa atg aag agt cca gaa aag aag cga agg aag tca aat act	322
Gly Leu Gln Met Lys Ser Pro Glu Lys Arg Arg Lys Ser Asn Thr	
35 40 45 50	
cag ggc cct gca tac tca cat ctg acg gag ttt gca cca ccc cca act	370
Gln Gly Pro Ala Tyr Ser His Leu Thr Glu Phe Ala Pro Pro Pro Thr	
55 60 65	
ccc atg gtg gat cac ctg gtt gca tcc aac cct ttt gaa gat gac ttc	418
Pro Met Val Asp His Leu Val Ala Ser Asn Pro Phe Glu Asp Asp Phe	
70 75 80	

gga gcc ccc aaa gtg ggg gtt gca gcc cct cca ttc ctt ggc agt cct	466
Gly Ala Pro Lys Val Gly Val Ala Ala Pro Pro Phe Leu Gly Ser Pro	
85 90 95	
gtg ccc ttc gga ggc ttc cgt gtg cag ggg ggc atg gcg ggc cag gta	514
Val Pro Phe Gly Gly Phe Arg Val Gln Gly Gly Met Ala Gly Gln Val	
100 105 110	
ccc cca ggc tac agc act gga ggt gga ggg ggc ccc cag cca ctc cgt	562
Pro Pro Gly Tyr Ser Thr Gly Gly Gly Pro Gln Pro Leu Arg	
115 120 125 130	
cga cag cca ccc ccc ttc cct ccc aat cct atg ggc cct gct ttc aac	610
Arg Gln Pro Pro Pro Phe Pro Pro Asn Pro Met Gly Pro Ala Phe Asn	
135 140 145	
atg ccc ccc cag ggt cct ggc tac cca ccc cca ggc aac atg aac ttt	658
Met Pro Pro Gln Gly Pro Gly Tyr Pro Pro Pro Gly Asn Met Asn Phe	
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ccc agc caa ccc ttc aac cag cct ctg ggt caa aac ttt agt cct ccc	706
Pro Ser Gln Pro Phe Asn Gln Pro Leu Gly Gln Asn Phe Ser Pro Pro	
165 170 175	
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Ser Gly Gln Met Met Pro Gly Pro Val Gly Gly Phe Gly Pro Met Ile	
180 185 190	
tca ccc acc atg gga cag cct ccc aga gca gag ctg ggc cca cct tct	802
Ser Pro Thr Met Gly Gln Pro Pro Arg Ala Glu Leu Gly Pro Pro Ser	
195 200 205 210	
ctg tcc caa cga ttt gct cag cca ggg gct cct ttt ggc cct tct cct	850
Leu Ser Gln Arg Phe Ala Gln Pro Gly Ala Pro Phe Gly Pro Ser Pro	
215 220 225	
ctc cag aga cct ggt cag ggg ctc ccc agc ctg ccg cct aac aca agt	898
Leu Gln Arg Pro Gly Gln Gly Leu Pro Ser Leu Pro Pro Asn Thr Ser	
230 235 240	
ccc ttt cct ggt ccg gac cct ggc ttt cct ggc cct ggt ggt gag gat	946
Pro Phe Pro Gly Pro Asp Pro Gly Phe Pro Gly Pro Gly Glu Asp	
245 250 255	
ggg ggg aag ccc ttg aat cca cct gct tct act gct ttt ccc cag gag	994
Gly Gly Lys Pro Leu Asn Pro Pro Ala Ser Thr Ala Phe Pro Gln Glu	
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ccc cac tca ggc tcc ccg gct gct gct gtt aat ggg aac cag ccc agt	1042
Pro His Ser Gly Ser Pro Ala Ala Val Asn Gly Asn Gln Pro Ser	
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tcc ccc ccg aac agc agt ggg cgg ggt ggg ggc act cca gat gcc aac	1090
Phe Pro Pro Asn Ser Ser Gly Arg Gly Gly Thr Pro Asp Ala Asn	
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Ser Leu Ala Pro Pro Gly Lys Ala Gly Gly Ser Gly Pro Gln Pro	
310 315 320	

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Asp Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser Cys Gln Lys Trp Phe	
340 345 350	
cac cgt gag tgc aca ggc atg act gag agc gcc tat ggg ctg ctg acc	1282
His Arg Glu Cys Thr Gly Met Thr Glu Ser Ala Tyr Gly Leu Leu Thr	
355 360 365 370	
act gaa gct tct gcc gtc tgg gcc tgc gat ctc tgc ctc aag acc aag	1330
Thr Glu Ala Ser Ala Val Trp Ala Cys Asp Leu Cys Leu Lys Thr Lys	
375 380 385	
gag atc cag tct gtc tac atc cgt gag ggc atg ggg cag ctg gtg gct	1378
Glu Ile Gln Ser Val Tyr Ile Arg Glu Gly Met Gly Gln Leu Val Ala	
390 395 400	
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Ala Asn Asp Gly	
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tgctcttcca gggtgatttt ttgtatgttt ggctcttggc cttgtttcc actggctttc	1493
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<223> hPygo-2

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20 25 30  
  
Lys Ala Gly Leu Gln Met Lys Ser Pro Glu Lys Lys Arg Arg Lys Ser  
35 40 45  
  
Asn Thr Gln Gly Pro Ala Tyr Ser His Leu Thr Glu Phe Ala Pro Pro  
50 55 60  
  
Pro Thr Pro Met Val Asp His Leu Val Ala Ser Asn Pro Phe Glu Asp  
65 70 75 80  
  
Asp Phe Gly Ala Pro Lys Val Gly Val Ala Ala Pro Pro Phe Leu Gly  
85 90 95  
  
Ser Pro Val Pro Phe Gly Gly Phe Arg Val Gln Gly Gly Met Ala Gly  
100 105 110  
  
Gln Val Pro Pro Gly Tyr Ser Thr Gly Gly Gly Gly Pro Gln Pro  
115 120 125  
  
Leu Arg Arg Gln Pro Pro Pro Phe Pro Pro Asn Pro Met Gly Pro Ala  
130 135 140  
  
Phe Asn Met Pro Pro Gln Gly Pro Gly Tyr Pro Pro Pro Gly Asn Met  
145 150 155 160  
  
Asn Phe Pro Ser Gln Pro Phe Asn Gln Pro Leu Gly Gln Asn Phe Ser  
165 170 175  
  
Pro Pro Ser Gly Gln Met Met Pro Gly Pro Val Gly Gly Phe Gly Pro  
180 185 190  
  
Met Ile Ser Pro Thr Met Gly Gln Pro Pro Arg Ala Glu Leu Gly Pro  
195 200 205  
  
Pro Ser Leu Ser Gln Arg Phe Ala Gln Pro Gly Ala Pro Phe Gly Pro  
210 215 220  
  
Ser Pro Leu Gln Arg Pro Gly Gln Gly Leu Pro Ser Leu Pro Pro Asn  
225 230 235 240  
  
Thr Ser Pro Phe Pro Gly Pro Asp Pro Gly Phe Pro Gly Pro Gly Gly  
245 250 255  
  
Glu Asp Gly Gly Lys Pro Leu Asn Pro Pro Ala Ser Thr Ala Phe Pro  
260 265 270  
  
Gln Glu Pro His Ser Gly Ser Pro Ala Ala Ala Val Asn Gly Asn Gln  
275 280 285  
  
Pro Ser Phe Pro Pro Asn Ser Ser Gly Arg Gly Gly Gly Thr Pro Asp  
290 295 300

Ala Asn Ser Leu Ala Pro Pro Gly Lys Ala Gly Gly Gly Ser Gly Pro  
 305 310 315 320  
 Gln Pro Pro Pro Gly Leu Val Tyr Pro Cys Gly Ala Cys Arg Ser Glu  
 325 330 335  
 Val Asn Asp Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser Cys Gln Lys  
 340 345 350  
 Trp Phe His Arg Glu Cys Thr Gly Met Thr Glu Ser Ala Tyr Gly Leu  
 355 360 365  
 Leu Thr Thr Glu Ala Ser Ala Val Trp Ala Cys Asp Leu Cys Leu Lys  
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 Val Ala Ala Asn Asp Gly  
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 Gly Gly Asp Ser Gly Leu Asp Gly Leu Gly Gly Pro Gly Val Gln Leu  
 20 25 30

gga agc cca gat aag aag cgc aag gca aat aca cag gga cct tct 144  
 Gly Ser Pro Asp Lys Lys Arg Lys Ala Asn Thr Gln Gly Pro Ser  
 35 40 45

ttc cct cca ttg tct gag tat gct cca cca ccg aat cca aac tct gac 192  
 Phe Pro Pro Leu Ser Glu Tyr Ala Pro Pro Pro Asn Pro Asn Ser Asp  
 50 55 60

cat cta gtg gct gct aat cca ttt gat gac aac tat aat act att tcc 240  
 His Leu Val Ala Ala Asn Pro Phe Asp Asp Asn Tyr Asn Thr Ile Ser  
 65 70 75 80

tat aaa cca cta cct tcg tca aat cca tat ctt ggc cct ggt tat cct 288  
 Tyr Lys Pro Leu Pro Ser Ser Asn Pro Tyr Leu Gly Pro Gly Tyr Pro  
 85 90 95

ggc ttt gga ggc tat agt aca ttc aga atg cca cct cac gtt ccc cca Gly Phe Gly Gly Tyr Ser Thr Phe Arg Met Pro Pro His Val Pro Pro 100 105 110	336
aga atg tct tcc cca tac tgt ggt cct tac tca ctc agg aac cag cca Arg Met Ser Ser Pro Tyr Cys Gly Pro Tyr Ser Leu Arg Asn Gln Pro 115 120 125	384
cac cca ttt cct cag aat cct ctg ggc atg ggt ttt aat cga cct cat His Pro Phe Pro Gln Asn Pro Leu Gly Met Gly Phe Asn Arg Pro His 130 135 140	432
gct ttt aac ttt ggg cca cat gat aat tca agt ttc ggt aat cca tct Ala Phe Asn Phe Gly Pro His Asp Asn Ser Ser Phe Gly Asn Pro Ser 145 150 155 160	480
tat aat aat gca cta agt cag aat gtc aac atg cct aat caa cat ttt Tyr Asn Asn Ala Leu Ser Gln Asn Val Asn Met Pro Asn Gln His Phe 165 170 175	528
aga caa aat cct gct gaa aat ttc agt caa att cct cca cag aat gct Arg Gln Asn Pro Ala Glu Asn Phe Ser Gln Ile Pro Pro Gln Asn Ala 180 185 190	576
agc caa gtt tct aac ccc gat ttg gca tct aat ttt gtt cct gga aat Ser Gln Val Ser Asn Pro Asp Leu Ala Ser Asn Phe Val Pro Gly Asn 195 200 205	624
aat tca aat ttt act tct ccg tta gaa tct aat cat tct ttt att cct Asn Ser Asn Phe Thr Ser Pro Leu Glu Ser Asn His Ser Phe Ile Pro 210 215 220	672
ccc cca aac act ttt ggt caa gca aaa gca cca ccc cca aaa caa gac Pro Pro Asn Thr Phe Gly Gln Ala Lys Ala Pro Pro Pro Lys Gln Asp 225 230 235 240	720
ttt act caa gga gca acc aaa aac act aat caa aat tcc tct gct cat Phe Thr Gln Gly Ala Thr Lys Asn Thr Asn Gln Asn Ser Ser Ala His 245 250 255	768
cca cct cac ttg aat atg gat gac aca gtg aat cag agt aat att gaa Pro Pro His Leu Asn Met Asp Asp Thr Val Asn Gln Ser Asn Ile Glu 260 265 270	816
tta aaa aat gtt aat cga aac aat gca gta aat cag gag aac agc cgt Leu Lys Asn Val Asn Arg Asn Asn Ala Val Asn Gln Glu Asn Ser Arg 275 280 285	864
tca agt agc act gaa gcc aca aac aat aac cct gca aat ggg acg cag Ser Ser Ser Thr Glu Ala Thr Asn Asn Pro Ala Asn Gly Thr Gln 290 295 300	912
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Ser Asp Pro Val Tyr Pro Cys Gly Ile Cys Thr Asn Glu Val Asn Asp	
340 345 350	
gat cag gat gcc atc tta tgt gag gcc tct tgt cag aaa tgg ttt cat	1104
Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser Cys Gln Lys Trp Phe His	
355 360 365	
cgg atc tgt act gga atg act gaa aca gct tat ggc ctc tta act gca	1152
Arg Ile Cys Thr Gly Met Thr Glu Thr Ala Tyr Gly Leu Leu Thr Ala	
370 375 380	
gaa gca tct gca gta tgg ggc tgt gat acc tgt atg gct gac aaa gat	1200
Glu Ala Ser Ala Val Trp Gly Cys Asp Thr Cys Met Ala Asp Lys Asp	
385 390 395 400	
gtc cag tta atg cgt act aga gaa act ttt ggt cca tct gca gtg ggc	1248
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35 40 45	
Phe Pro Pro Leu Ser Glu Tyr Ala Pro Pro Pro Asn Pro Asn Ser Asp	
50 55 60	
His Leu Val Ala Ala Asn Pro Phe Asp Asp Asn Tyr Asn Thr Ile Ser	
65 70 75 80	
Tyr Lys Pro Leu Pro Ser Ser Asn Pro Tyr Leu Gly Pro Gly Tyr Pro	
85 90 95	
Gly Phe Gly Gly Tyr Ser Thr Phe Arg Met Pro Pro His Val Pro Pro	
100 105 110	
Arg Met Ser Ser Pro Tyr Cys Gly Pro Tyr Ser Leu Arg Asn Gln Pro	
115 120 125	
His Pro Phe Pro Gln Asn Pro Leu Gly Met Gly Phe Asn Arg Pro His	
130 135 140	

Ala Phe Asn Phe Gly Pro His Asp Asn Ser Ser Phe Gly Asn Pro Ser  
 145 150 155 160

Tyr Asn Asn Ala Leu Ser Gln Asn Val Asn Met Pro Asn Gln His Phe  
 165 170 175

Arg Gln Asn Pro Ala Glu Asn Phe Ser Gln Ile Pro Pro Gln Asn Ala  
 180 185 190

Ser Gln Val Ser Asn Pro Asp Leu Ala Ser Asn Phe Val Pro Gly Asn  
 195 200 205

Asn Ser Asn Phe Thr Ser Pro Leu Glu Ser Asn His Ser Phe Ile Pro  
 210 215 220

Pro Pro Asn Thr Phe Gly Gln Ala Lys Ala Pro Pro Pro Lys Gln Asp  
 225 230 235 240

Phe Thr Gln Gly Ala Thr Lys Asn Thr Asn Gln Asn Ser Ser Ala His  
 245 250 255

Pro Pro His Leu Asn Met Asp Asp Thr Val Asn Gln Ser Asn Ile Glu  
 260 265 270

Leu Lys Asn Val Asn Arg Asn Asn Ala Val Asn Gln Glu Asn Ser Arg  
 275 280 285

Ser Ser Ser Thr Glu Ala Thr Asn Asn Asn Pro Ala Asn Gly Thr Gln  
 290 295 300

Asn Lys Pro Arg Gln Pro Arg Gly Ala Ala Asp Ala Cys Thr Thr Glu  
 305 310 315 320

Lys Ser Asn Lys Ser Ser Leu His Pro Asn Arg His Gly His Ser Ser  
 325 330 335

Ser Asp Pro Val Tyr Pro Cys Gly Ile Cys Thr Asn Glu Val Asn Asp  
 340 345 350

Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser Cys Gln Lys Trp Phe His  
 355 360 365

Arg Ile Cys Thr Gly Met Thr Glu Thr Ala Tyr Gly Leu Leu Thr Ala  
 370 375 380

Glu Ala Ser Ala Val Trp Gly Cys Asp Thr Cys Met Ala Asp Lys Asp  
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Val Gln Leu Met Arg Thr Arg Glu Thr Phe Gly Pro Ser Ala Val Gly  
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<220>  
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<400> 7  
ccacccctt ccagttgtc c 21

<210> 8  
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<210> 9  
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<210> 12  
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<210> 13  
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<400> 13  
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<223> Hpy2A siRNA

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<210> 16  
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<223> Hpy2B siRNA

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agaagcgaag gaagucaaa 19

<210> 17  
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<223> Hpy2C siRNA

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<210> 18  
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<210> 19  
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<210> 23  
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<220>  
<223> Reverse hPygo2 primer

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<210> 24  
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<220>  
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<400> 24  
gccacgacaa ccaagagg 20

<210> 25  
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<210> 26  
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<220>  
<223> Forward Bcl-9 primer

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<210> 27  
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<212> DNA  
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<220>  
<223> Reverse Bcl-9 primer

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<210> 28  
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<220>  
<223> mismatched sequence to Hpy5

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